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GENETIC VARIATION OF *TRICHURIS* SPP. OBTAINED FROM HUMANS AND PIGS

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The whipworms *Trichuris trichiura* and *T. suis* in humans and pigs, respectively, are believed to be closely related but different species. The aim of our study was to examine the genetic variation of *Trichuris* spp. recovered from pigs and humans. Initially, sympatric worm material isolated from 10 humans and 5 pigs in Uganda supplemented with pig *Trichuris* from Tanzania, Denmark and USA and a human worm from Jamaica, was included. For 20 worms the second internal transcribed spacer (ITS-2) in the r-DNA was amplified by PCR and cloned. 49 human and 45 pig-derived clones were sequenced and allocated into 56 different haplotypes. A very large intra-individual variation was found within the human-derived sequences (0.2 – 45.0%) compared to the pig derived sequences (0.2 – 1.4%). This was due to two main ITS-2 sequence types in the human-derived worms; a type 1 being unique to human-derived worms and a type 2 being identical to the sequence type found in pig-derived worms. Subsequently, the sequence information was used to develop a PCR-linked Restriction Fragment Length Polymorphism (PCR-RFLP) that could identify these genotypes. The method was applied on the above mentioned material and on additional worms obtained from pigs collected in Uganda, USA, Tanzania, Jamaica and Denmark as well as worms from humans in Uganda, Jamaica and China. The distribution of the three genotypes (type 1, type 2 and 'heterozygote') was 2, 57 and 0, respectively, in 59 worms recovered from pigs and 26, 1 and 2, respectively, in 29 worms recovered from human. These results clearly suggest that *Trichuris* in humans and pigs belong to two different populations ($\chi^2 = 49.5$; $P < 0.001$). However, we have also found evidence for a few cases of cross-infections and the existence of heterozygote worms, the latter suggesting cases of hybridization or retention of ancestral polymorphism.



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